

## SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Inze, Dirk  
Segers, Gerda  
De Veylder, Lieven  
Mironov, Vladimir
- (ii) TITLE OF INVENTION: METHOD AND MEANS FOR MODULATING  
PLANT CELL CYCLE PROTEINS AND THEIR USE IN PLANT  
CELL GROWTH AND CONTROL
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS
  - (A) ADDRESSEE: Nixon Peabody LLP
  - (B) STREET: 990 Stewart Avenue
  - (C) CITY: Garden City
  - (D) STATE: New York, New York
  - (E) ZIP: 11530
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: EP PCT/EP98/01522
  - (B) FILING DATE: 13-MAR-1998
  - (A) APPLICATION NUMBER: EP 97.200.765.2
  - (B) FILING DATE: 14-MAR-1997

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 454 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Arabidopsis thaliana
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 15..276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCTCTGAGAG AGAA ATG GGT CAG ATC CAA TAC TCC GAG AAA TAC TTC GAT Met Gly Gln Ile Gln Tyr Ser Glu Lys Tyr Phe Asp	50
1 5 10	
GAC ACT TTC GAA TAC AGG CAC GTC GTT CCT CCT GAA GTC GCT AAA Asp Thr Phe Glu Tyr Arg His Val Val Leu Pro Pro Glu Val Ala Lys	98
15 20 25	
CTT CTT CCA AAG AAT CGT CTT CTC TCC GAA AAC GAA TGG CGA GCG ATA Leu Leu Pro Lys Asn Arg Leu Leu Ser Glu Asn Glu Trp Arg Ala Ile	146
30 35 40	
GGA GTG CAG CAA AGC CGC GGA TGG GTA CAT TAC GCG GTT CAT CGA CCT Gly Val Gln Gln Ser Arg Gly Trp Val His Tyr Ala Val His Arg Pro	194
45 50 55 60	
GAG CCG CAC ATA ATG CTA TTC AGG AGG CCT CTT AAC TAT CAG CAG CAG Glu Pro His Ile Met Leu Phe Arg Arg Pro Leu Asn Tyr Gln Gln Gln	242
65 70 75	
CAG GAG AAT CAA GCT CAG AAC ATG CTT GTT AAG T GAATCATTAT Gln Glu Asn Gln Ala Gln Asn Met Leu Val Lys	286
80 85	
CATCACCTGA GTAAGAACATGT TATATGCAAC AATTCTATGA GTATTGGTTT ATGTTCTTG	346
TAAACATGGT TTGAATCTTT GTGGTTATGG ATGAATATGT GAGAGTTGGT TTGTTGAACA	406
ACTTCTATGT AATGTTAGTC TTGGTTCTAA TGTCATCTTC TGCTTCTC	454

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGGGTCAGA TCCAATACTC CGAGAAATAC TTGATGACA CTTTCGAATA CAGGTAAAGC TCTTCAATCT CGCTTCTTCT TCCTCCAATT TTCACTCTCA CTTCTCTAAT CGTAATCGAT	60
CGATACAGGC ACGTCGTTCT TCCTCCTGAA GTCGCTAAC TTCTTCCAAA GAATCGTCTT	120
CTCTCCGAAG TAAGTTTTT TCCGCATTGT TCTCTGATTT CTGATTCTAA ATCCTTCGAT	180
TAGATCATCG AAGACTATGA AAATTTGTTG CTCTTAAGAA ATTAAGTTG GGAAAAATCG	240
	300

AAAAAAGAGAT CGTTTAGGTT TAGGATTGTA ATCTTGCTC TGAATCCAAA TTGCAACTGT	360
TACGATTTG AATCTTGCT TTGGGATTTT GTAAGGTTA GTGATAAAGA GATTTAGAC	420
ATTTGTGTTG TGCAATCTCT TCAATGTTGT ATTGATTGGT GGTGATGGTA AAAATGTTG	480
GAATTCGAA GAACGAATGG CGAGCGATAG GAGTGCAGCA AAGCCGCGGA TGGGTACATT	540
ACCGGGTTCA TCGACCTGAG CCGCACATAA TGCTATTCAAG GAGGCCTCTT AACTATCAGC	600
AGCAGCAGGA GAATCAAGCT CAGAACATGC TTGTTAAGTG AATCATTATC ATCACCTGAG	660
TAAGAATGTT ATATGCAACA GATCTATGAG TATTGG	696

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met	Gly	Gln	Ile	Gln	Tyr	Ser	Glu	Lys	Tyr	Phe	Asp	Asp	Thr	Phe	Glu
1					5				10					15	

Tyr	Arg	His	Val	Val	Leu	Pro	Pro	Glu	Val	Ala	Lys	Leu	Leu	Pro	Lys
					20				25				30		

Asn	Arg	Leu	Leu	Ser	Glu	Asn	Glu	Trp	Arg	Ala	Ile	Gly	Val	Gln	Gln
					35			40				45			

Ser	Arg	Gly	Trp	Val	His	Tyr	Ala	Val	His	Arg	Pro	Glu	Pro	His	Ile
					50			55			60				

Met	Leu	Phe	Arg	Arg	Pro	Leu	Asn	Tyr	Gln	Gln	Gln	Glu	Asn	Gln
65					70				75			80		

Ala	Gln	Asn	Met	Leu	Val	Lys									
					85										

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Gly Gln Ile Gln Tyr Ser Glu Lys Tyr Phe Asp Asp Thr Phe Glu  
1                   5                   10                   15

Tyr Arg His Val Val Leu Pro Pro Glu Val Ala Lys Leu Leu Pro Lys  
20                   25                   30

Asn Arg Leu Leu Ser Glu Asn Glu Trp Arg Ala Ile Gly Val Gln Gln  
35                   40                   45

Ser Arg Gly Trp Val His Tyr Ala Val His Arg Pro Glu Pro His Ile  
50                   55                   60

Met Leu Phe Arg Arg Pro Leu Asn  
65                   70